

1/26

TWIK 2

Input file FthKa020g04.seq; Output File FthKa020g04.tra
Sequence length 3452

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I  G  A  A  I  F  E  V  L  E  E  P  H  W  K  E  A  K  K  N
ATC GGG GCG GCG ATC TTC GAA GTG CTG GAG GAG CCA CAC TGG AAG GAG GCC AAG AAA AAC
Y  Y  T  Q  K  L  H  L  L  K  E  F  P  C  L  G  Q  E  G  L
TAC TAC ACA CAG AAG CTG CAT CTG CTC AAG GAG TTC CCG TGC CTG GGT CAG GAG GGC CTG
D  K  I  L  E  V  V  S  D  A  A  G  Q  G  V  A  I  T  G  N
GAC AAG ATC CTA GAG GTG GTA TCT GAT GCT GCA GGA CAG GGT GTG GCC ATC ACA GGG AAC
Q  T  F  N  N  W  N  W  P  N  A  M  I  F  A  A  T  V  I  T
CAG ACC TTC AAC AAC TGG AAC TGG CCC AAT GCA ATG ATT TTT GCA GCG ACC GTC ATT ACC
T  I  G  Y  G  N  V  A  P  K  T  P  A  G  R  L  F  C  V  F
ACC ATT GGA TAT GGC AAT GTG GCT CCC AAG ACC CCC GCC GGT CGC CTC TTC TGT GTT TTC
Y  G  L  F  G  V  P  L  C  L  T  W  I  S  A  L  G  K  F  F
TAT GGT CTC TTC GGG GTG CCG CTC TGC CTG ACG TGG ATC AGT GCC CTG GGC AAG TTC TTC
G  G  R  A  K  R  L  G  Q  F  L  T  K  R  G  V  S  L  R  K
GGG GGA CGT GCC AAG AGA CTA GGG CAG TTC CTT ACC AAG AGA GGT GTG AGT CTG CGG AAG
A  Q  I  T  C  T  V  I  F  I  V  W  G  V  L  V  H  L  V  I
GCG CAG ATC ACG TGC ACA GTC ATC TTC ATC GTG TGG GGC GTC CTA GTC CAC CTG GTG ATC
P  P  F  V  F  M  V  T  E  G  W  N  Y  I  E  G  L  Y  Y  S
CCA CCC TTC GTA TTC ATG GTG ACT GAG GGG TGG AAC TAC ATC GAG GGC CTC TAC TAC TCC
F  I  T  I  S  T  I  G  F  G  D  F  V  A  G  V  N  P  S  A
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N  Y  H  A  L  Y  R  Y  F  V  E  L  W  I  Y  L  G  L  A  W
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L  S  L  F  V  N  W  K  V  S  M  F  V  E  V  H  K  A  I  K
CTG TCC CTT TTT GTC AAC TGG AAG GTG AGC ATG TTT GTG GAA GTC CAC AAA GCC ATT AAG
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Q  V  K  G  S  T  A  S  K  D  V  N  I  F  S  F  L  S  K  K
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E  E  T  Y  N  D  L  I  K  Q  I  G  K  K  A  M  K  T  S  G
GAA GAG ACC TAC AAC GAC CTC ATC AAG CAG ATC GGG AAG AAG GCC ATG AAG ACA AGC GGG
G  G  E  T  G  P  G  P  G  L  G  P  Q  G  G  G  L  P  A  L
GGT GGG GAG ACG GGC CCG GGC CCA GGG CTG GGG CCT CAA GGC GGT GGG CTC CCA GCA CTG
P  P  S  L  V  P  L  V  V  Y  S  K  N  R  V  P  T  L  E  E
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V  S  Q  T  L  R  S  K  G  H  V  S  R  S  P  D  E  E  A  V
GTG TCA CAG ACA CTG AGG AGC AAA GGC CAC GTA TCA AGG TCC CCA GAT GAG GAG GCT GTG
A  R  A  P  E  D  S  S  P  A  P  E  V  F  M  N  Q  L  D  R
GCA CGG GCC CCT GAA GAC AGC TCC CCT GCC CCC GAG GTG TTC ATG AAC CAG CTG GAC CGC
I  S  E  E  C  E  P  W  D  A  Q  D  Y  H  P  L  I  F  Q  D
ATC AGC GAG GAA TGC GAG CCA TGG GAC GCC CAG GAC TAC CAC CCA CTC ATC TTC CAG GAC
A  S  I  T  F  V  N  T  E  A  G  L  S  D  E  E  T  S  K  S
GCC AGC ATC ACC TTC GTG AAC ACG GAG GCT GGC CTC TCA GAC GAG GAG ACC TCC AAG TCC
S  L  E  D  N  L  A  G  E  E  S  P  Q  Q  G  A  E  A  K  A
TCG CTA GAG GAC AAC TTG GCA GGG GAG GAG AGC CCC CAG CAG GGG GCT GAA GCC AAG GCG
```

Fig. 1

P L N M G E F P S S S E S T F T S T E S
CCC CTG AAC ATG GGC GAG TTC CCC TCC TCC TCC GAG TCC ACC TTC ACC AGC ACT GAG TCT
E L S V P Y E Q L M N E Y N K A N S P K
GAG CTC TCT GTG CCT TAC GAA CAG CTG ATG AAT GAG TAC AAC AAG GCT AAC AGC CCC AAG
G T *
GGC ACA TGA

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ACTGCTGTTTTTATATACCTGGAATCTGTTGTTGGCTTCAGAGCCAGTGGTTAAAGAGCAGGGTCCCAAGGATTGGGAG
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Fig. 1 (continued)

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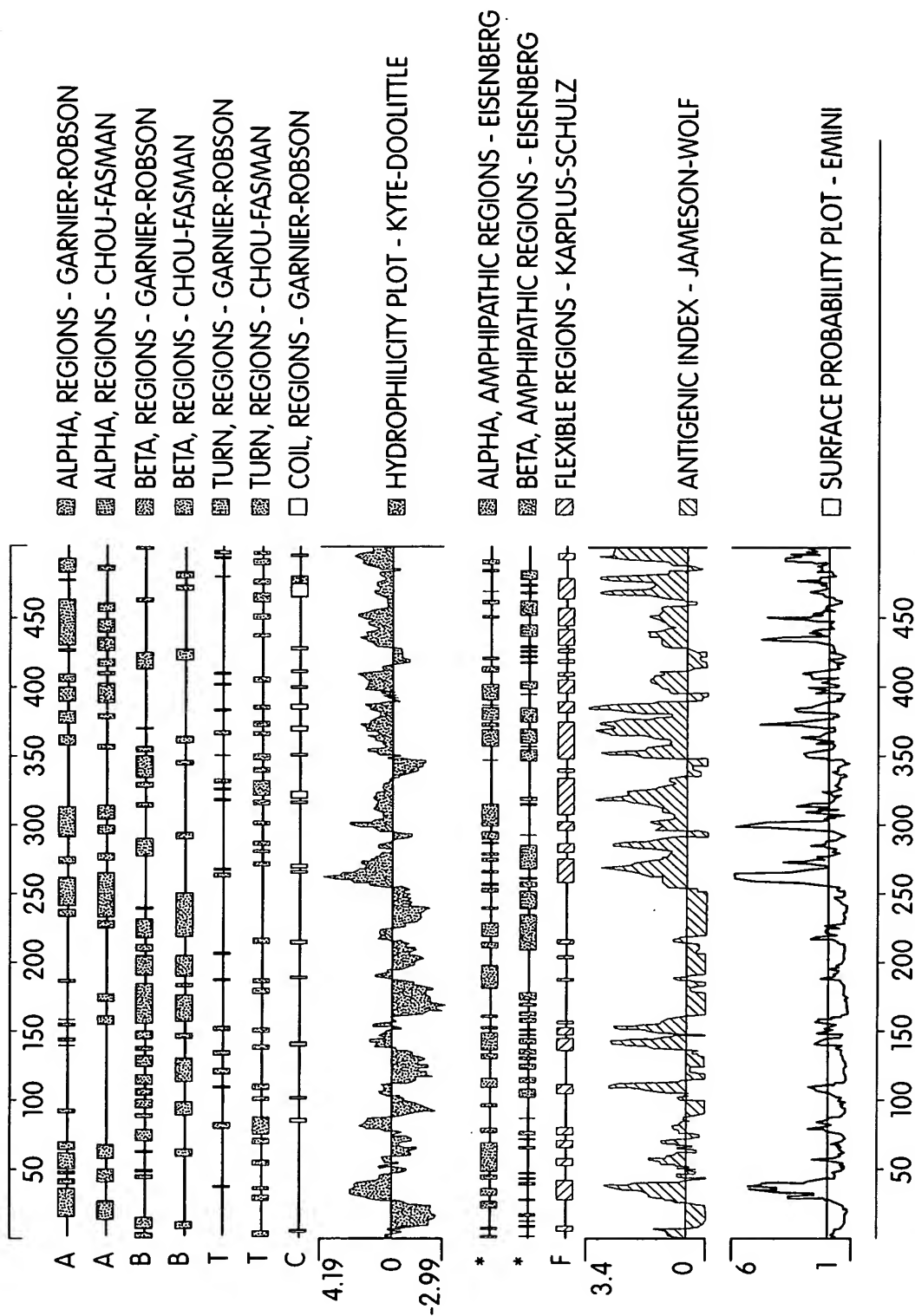


Fig. 2

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Input file Athua133f10.seq; Output File Athua133f10.tra
Sequence length 1575

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P E G R V R G C A V P G T V L L L L A Y
CCC GAG GGC AGG GTC CGG GGC TGC GCG GTG CCC GGC ACC GTG CTC CTG CTG CTC GCC TAC
L A Y L A L G T G V F W T L E G R A A Q
CTG GCT TAC CTG GCG CTG GGC ACC GGC GTG TTC TGG ACG CTG GAG GGC CGC GCG GCG CAG
D S S R S F Q R D K W E L L Q N F T C L
GAC TCC AGC CGC AGC TTC CAG CGC GAC AAG TGG GAG CTG TTG CAG AAC TTC ACG TGT CTG
D R P A L D S L I R D V V Q A Y K N G A
GAC CGC CCG GCG CTG GAC TCG CTG ATC CGG GAT GTC GTC CAA GCA TAC AAA AAC GGA GCC
S L L S N T T S M G R W E L V G S F F F
AGC CTC CTC AGC AAC ACC ACC AGC ATG GGG CGC TGG GAG CTC GTG GGC TCC TTC TTC TTT
S V S T I T T I G Y G N L S P N T M A A
TCT GTG TCC ACC ATC ACC ACC ATT GGC TAT GGC AAC CTG AGC CCC AAC ACG ATG GCT GCC
R L F C I F F A L V G I P L N L V V L N
CGC CTC TTC TGC ATC TTC TTT GCC CTT GTG GGG ATC CCA CTC AAC CTC GTG GTG CTC AAC
R L G H L M Q Q G V N H W A S R L G G T
CGA CTG GGG CAT CTC ATG CAG CAG GGA GTA AAC CAC TGG GCC AGC AGG CTG GGG GGC ACC
W Q D P D K A R W L A G S G A L L S G L
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L L F L L L P P L L F S H M E G W S Y T
CTG CTC TTC CTG CTG CTG CCA CCG CTG CTC TTC TCC CAC ATG GAG GGC TGG AGC TAC ACA
E G F Y F A F I T L S T V G F G D Y V I
GAG GGC TTC TAC TTC GCC TTC ATC ACC CTC AGC ACC GTG GGC TTC GGC GAC TAC GTG ATT
G M N P S Q R Y P L W Y K N M V S L W I
GGA ATG AAC CCC TCC CAG AGG TAC CCA CTG TGG TAC AAG AAC ATG GTG TCC CTG TGG ATC
L F G M A W L A L I I K L I L S Q L E T
CTC TTT GGG ATG GCA TGG CTG GCC TTG ATC ATC AAA CTC ATC CTC TCC CAG CTG GAG ACG
P G R V C S C C H H S S K E D F K S Q S
CCA GGG AGG GTA TGT TCC TGC TGC CAC CAC AGC TCT AAG GAA GAC TTC AAG TCC CAA AGC
W R Q G P D R E P E S H S P Q Q G C Y P
TGG AGA CAG GGA CCT GAC CGG GAG CCA GAG TCC CAC TCC CCA CAG CAA GGA TGC TAT CCA
E G P M G I I Q H L E P S A H A A G C G
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K D S *
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Fig. 3

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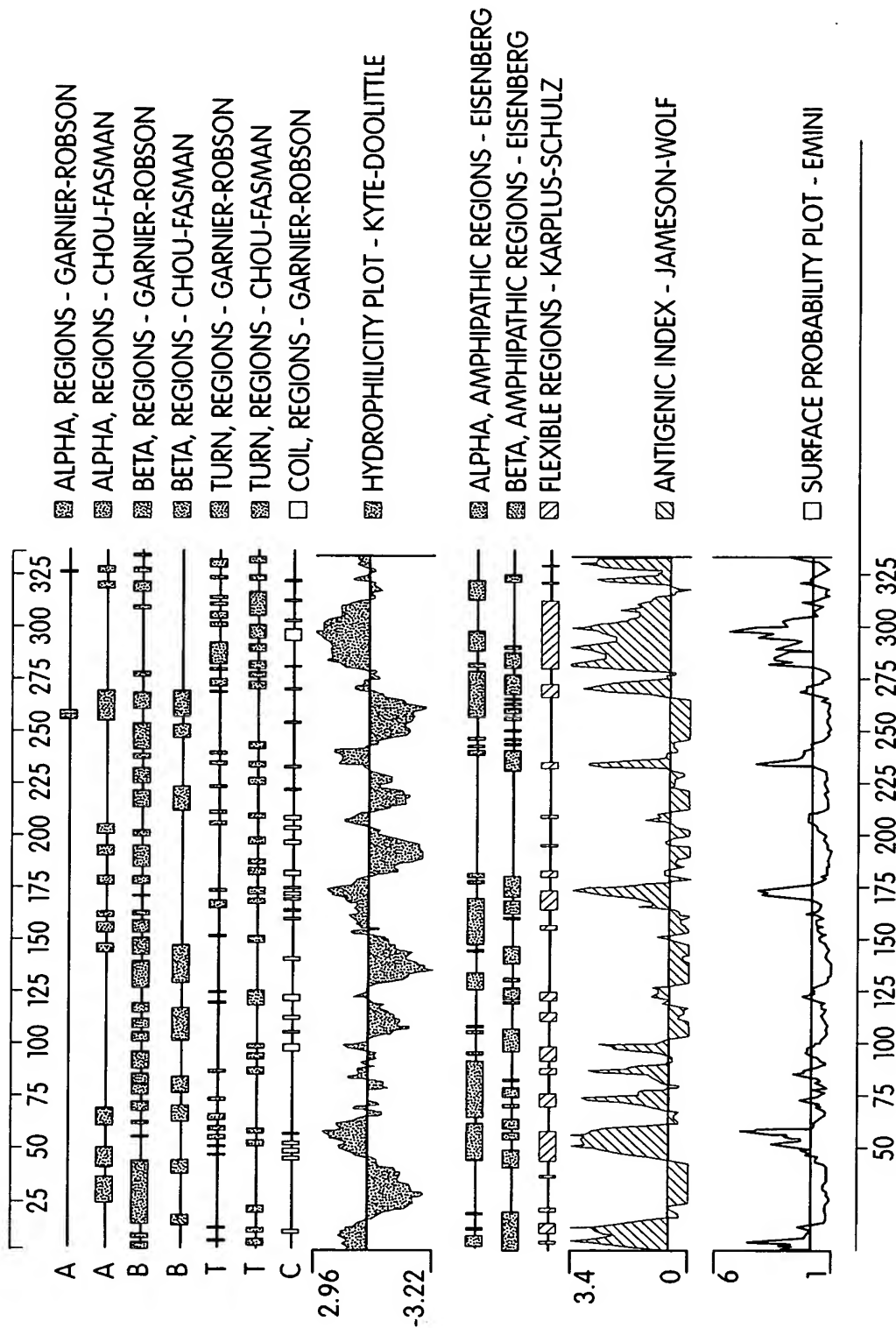


Fig. 4

TWIK 4

Input file AthTb005e07.seq; Output File AthTb005e07.tra

Sequence length 2287

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L L A G A L A A Y A A Y L V L G A L L V
CTT CTG GCG GGC GCC TTG GCC GCG TAC GCC GCG TAC CTG GTG CTG GGC GCG CTG TTG GTG
A R L E G P H E A R L R A E L E T L R A
GCG CGG CTG GAG GGG CCG CAC GAA GCC AGG CTC CGA GCC GAG CTG GAG ACG CTG CGG GCG
Q L L Q R S P C V A A P A L D A F V E R
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V L A A G R L G R V V L A N A S G S A N
GTG CTG GCG GCC GGA CGG CTG GGG CGG GTC GTG CTT GCT AAC GCT TCG GGG TCC GCC AAC
A S D P A W D F A S A L F F A S T L I T
GCC TCG GAC CCC GCC TGG GAC TTC GCC TCT GCT CTC TTC TTC GCC AGC ACG CTG ATC ACC
T V G Y G Y T T P L T D A G K A F S I A
ACC GTG GGC TAT GGG TAC ACA ACG CCA CTG ACT GAT GCG GGC AAG GCC TTC TCC ATC GCC
F A L L G V P T T M L L L T A S A Q R L
TTT GCG CTC CTG GGC GTG CCG ACC ACC ATG CTG CTG CTG ACC GCC TCA GCC CAG CGC CTG
S L L L T H V P L S W L S M R W G W D P
TCA CTG CTG CTG ACT CAC GTG CCC CTG TCT TGG CTG AGC ATG CGT TGG GGC TGG GAC CCC
R R A A C W H L V A L L G V V V T V C F
CGG CGG GCG GCC TGC TGG CAC TTG GTG GCC CTG TTG GGG GTC GTA GTG ACC GTC TGC TTT
L V P A V I F A H L E E A W S F L D A F
CTG GTG CCG GCT GTG ATC TTT GCC CAC CTC GAG GAG GCC TGG AGC TTC TTG GAT GCC TTC
Y F C F I S L S T I G L G D Y V P G E A
TAC TTC TGC TTT ATC TCT CTG TCC ACC ATC GGC CTG GGC GAC TAC GTG CCC GGG GAG GCC
P G Q P Y R A L Y K V L V T V Y L F L G
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L V A M V L V L Q T F R H V S D L H G L
CTG GTG GCC ATG GTG CTG GTG CTG CAG ACC TTC CGC CAC GTG TCC GAC CTC CAC GGC CTC
T E L I L L P P P C P A S F N A D E D D
ACG GAG CTC ATC CTG CTG CCC CCT CCG TGC CCT GCC AGT TTC AAT GCG GAT GAG GAC GAT
R V D I L G P Q P E S H Q Q L S A S S H
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T D Y A S I P R
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Fig. 5

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CCTGAANCTATGAGAAATAGGCAGGAAGAAGTTGTACCNTGACTCATTTTTTTTCAGGTGTCTCCAGGGAGCAGGACCCA
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Fig. 5 (continued)

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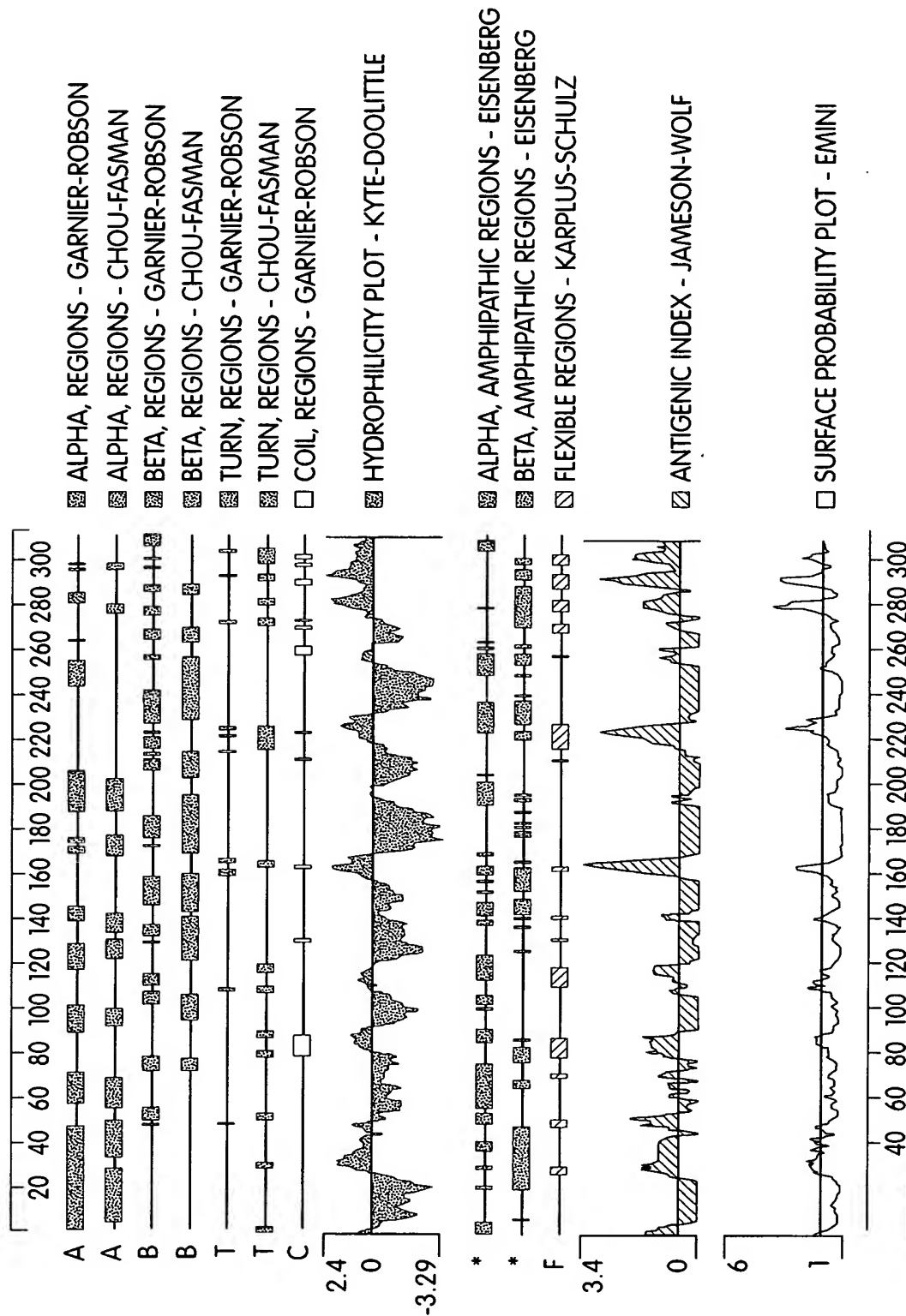


Fig. 6

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Clustal W (1.74) multiple sequence alignment

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mTREK-1 MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTSTIFLVVVLYLII
Athua133f10 -----MYRPRARAAPEGRVRGCAVPGTVLLLLLAY-----LAYLAL
FthKa20g4 -----MVDRGPLLTSIIF-----YLAI
hTASK -----MKRQNVRTLALIVC-----TFTYLLV
                                     : **

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mTREK-1 GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAINAGIIPLGNS
Athua133f10 GTGVFWTLEGRAAQDSSRSFQRDKWELLQNFTCLDRPALDSLIRDVVQAYKNGASLLSNT
FthKa20g4 GAAIFEVLEEPHWKEAKNYYTQKLHLLKEFPCLGQEGLDKILEVVSDAAGQGVAITGNQ
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FthKa20g4 TFN-N-----WNWPNAMIFAATVITTIGYGNVAPKTPAGRLFCVFGYGLFGVPLCLTWISA
hTASK -----WRFAGSFYFAITVITTIGYGHAA PSTDGGKVFCMFYALLGIPLTLVMFQS
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Athua133f10 SQLETPGRVCSCCHHSSKEDFK-----
FthKa20g4 SMFVEVHKAIAKKRRRRRRKESFESSPHSRKALQVKGSTASKDVNIFSFLSKKEETYNDLIK
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Fig. 7

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mTRAAK	-----SWTGTVTARVTQR-----T--
mTREK-1	-----EWTANVTAEFKETR----R--
Athua133f10	-----SQSWRQGPDREPES---HS--
FthKa20g4	QIGKKAMKTSGGGETGPGPGLGPQGGGLPALPPSLVPLVVYSKNRVPTLEEVSQTLRSKG
hTASK	-----GQAGGGGGGSAHTTDTAS--
AthTb005e07	-DILGPQPESHQQ---LSASSHTDYASIPR-----
hTWIK-1	-DQAAGMKEDQKQNEPFFVATQSSACVDGPANH-----
mTRAAK	-GPSAPPPEKEQPLLPSSLPAPPVVEPAGRPGSPA-PAEKVETPSPPTA-SALDYPSEN
mTREK-1	-RLSVEIYDKFQR---ATSVKRKLSAELAGNHNQELTPCMRTCL-----
Athua133f10	-PQQGCYPEGPMG--IIQHLEPSAHAAGCGKDS-----
FthKa20g4	HVSRSPDEEAVARAPEDSSPAPEVFMNQLDRISEECPWDAQDYHPLIFQ-DASITFVNT
hTASK	-STAAAGGGGFRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHS
AthTb005e07	-----
hTWIK-1	-----
mTRAAK	LAFIDESSDTQSERGCALPRAPGRRRPNPSKKPSRPRGPGRLRDKAVPV-----
mTREK-1	-----
Athua133f10	-----
FthKa20g4	EAGLSDEETSKSSLEDNLAGEESPQQGAEAKAPLNMGEFPSSSESTFTSTESELSVPYEQ
hTASK	SPGGGGGRYSDTPSRRCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV-----
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mTRAAK	-----
mTREK-1	-----
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Fig. 7 (continued)

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Clustal W (1.74) multiple sequence alignment

```
hTWIK-1      -----MLQSLAGSSCVRLVERHRSAWCFGFLVLG-----YLLYLVF
AthTb005e07  -----MRRGALLAGALAA-----YAAYLVL
mTRAAK       -----MRSTLLALLAL-----VLLYLVS
mTREK-1      MAAPDLLDPKSAAQNSKPRLSFSSKPTVLASRVESDSAINVMKWKTSTIFLVVLYLII
hTASK        -----MKRQNVRTLALIVC-----TFTYLLV
                  : . . . : **:
```

```
hTWIK-1      GAVVFSSVELPYEDLLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLEASNYGVSVLSNA
AthTb005e07  GALLVARLEGPEARLRAELETTLRAQLLQSPCVAAPALDAFVERVLAAGRLGRVVLANA
mTRAAK       GALVFQALEQPHEQQAQKMDHGRDQFLRDHPCVSQKSLEDFIKLLVEALGGGANPETS
mTREK-1      GAAVFKALEQPQEISQRTTIVIQKQTFIAQHACVNSTELDELIQQIVAAGIIPLGNS
hTASK        GAAVFDALASEPELIERQRLRLRQELRARYNLSQGGYEELERVVRLRKLPHKAGVQ---
** :. : * : : : : : : : : :
```

```
hTWIK-1      SGNWN-----WDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCIIYSVIGIPFTLLFLTA
AthTb005e07  SGSANASDPAWDFASALFFASTLITTVGYGYTTPLTDAGKAFSIAFALLGVPTTMLLLTA
mTRAAK       TNSSNHSS-AWNLGSAFFSGTITTTIGYGNIVLHTDAGRLFCIFYALVGIPFLFGMLLAG
mTREK-1      SNQVSH----WDLGSSFFFAAGTVITTTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLAG
hTASK        -----WRFAGSFYFAITVITTTIGYGHAAAPSTDGGKVFCMFYALLGIPLTLVMFQS
                  * : : : : * : : * : : : : * : : : : *
```

```
hTWIK-1      VVQRITVHVTR--RPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCFFFIPAAVFSVLEDD
AthTb005e07  SAQRSLSLLLTH--VPLSWLSMRWGWDPRRAACWHLVALLGVVTVCFVPAVIFAHLEEA
mTRAAK       VGDRLGSSSLRRGIGHIEAIFLKWHPVPGVLRSLSAVLFLIGCLLFVLTPTFVFSYMES-
mTREK-1      VGDQLGTIFGKGIKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLFVALPAVIFKHIEG-
hTASK        LGERINTLVRY---LLHRAKGLGMRRADVSMANMVLIGFFSCISTLCIGAAAFSHYEH-
                  : : . : : : : : : * *
```

```
hTWIK-1      WNFLESFYFCFISLSTIGLDYVPGEQYNQ-----KFRELYKIGITCYLLLGLIAMLVVL
AthTb005e07  WSFLDAFYFCFISLSTIGLDYVPGEAPGQ-----PYRALYKVLVBYLFLGLVAMVLVL
mTRAAK       WSKLEAIYFVIVTLTTVGFDYVPGDGTGQNS--PAYQPLVWFWILFGLAYFASVLTIG
mTREK-1      WSALDAIYFVIVTLTTIGFDYVAGGSDIEYL--DFYKPVVWFWILVGLAYFAAVLAMIG
hTASK        WFFFQAYYYCFITLTTIGFDYVALQKDQALQTQPOYVAFSFVYILTGLTVIGAFNLV
*. : : * : : : : : : : : : *
```

```
hTWIK-1      ETFCELHELKKFRKMFYVKKDK--DEDQVHIIHDQLSFSSITDQAAGMKEDQKQNEPFV
AthTb005e07  QTFRHVSDLHGLTELILLPPP--CPASFNADDDR-----DILGPQPEHQ--LS
mTRAAK       NWLRAVSRRTAEMGGLTAQAA--SWTGTVTARVTQR-----TGPSAPPEKEQPLPSS
mTREK-1      DWLRVISKKTKEEVGEFRAHAA--EWTANVTAEFKETR----RRLSVEIYDKFQR--AT
hTASK        LRFMTMNAEDEKRDAEHRALLTRNGQAGGGGGGSAHTTDTASSTAAGGGGTRNVYAEV
                  : : :
```

```
hTWIK-1      ATQSSACVDGPANH-----
AthTb005e07  ASSHTDYASIPR-----
mTRAAK       LPAPPVVEPAGRPGSPA-PAEKVETPSPTASALDYPSENLA-FIDESSDTQSERGCAL
mTREK-1      SVKRKLSAELAGNHNQELTPCMRTCL-----
hTASK        LHFQSMCSCSLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGGGRYSDTPSRRLC
```

```
hTWIK-1      -----
AthTb005e07  -----
mTRAAK       PRAPRGRRRPNPSKKPSRPRGPGRLRDKAVPV
mTREK-1      -----
hTASK        SGAPRSAISSVSTGLHSLSTFRGLMKRRSSV-
```

Fig. 8

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Clustal w (1.74) multiple sequence alignment

```

                                          TM 1
Athua133f10  -MYRPRARAAPEGRVRCVPGTVLLLLLAYLAYLALGTGVFWTLEGRAAQDSSRSFQRDK
h TASK2      -----MVDRGPLLTSAIFYLAIGAAIFEVLEEPHWKEAKNYYTQK
hTWIK-1      MLQSLAGSSCVRLVERHRSACWCFGLVLGYLLYLVFGAVVFSSVELPYEDLLRQELRKLK
hTASK        -----MKRQNVRTLALIVCTFTYLLVGAAVFDALESEPE-LIERQRLELR
                        *   : ** .*: :* :*   :
                                          P-LOOP 1
Athua133f10  WELLQNFTCLDRPALDSLIRDVVQAYKNGASLLSNTTSMGRWELVGSFFFSVSTITTIGY
h TASK2      LLLLKEFPCLGQEGLDKILEVVSDAAGQGVAITGNQTFNN-WNWPNAMIFAATVITTIGY
hTWIK-1      RRFLEEHECLSEQQLEQFLGRVLEASNYGVSVLSNASGNWNWDFTSALFFASTVLSTTGY
hTASK        QQELRARYNLSQGGYEELERVVLRRLKPH---KAGVQ-----WRFAGSFYFAITVITTIGY
                . * .   *..   :.:   *           *   .: : * : :.: * **
                        TM 2
Athua133f10  GNLSPTMAARLFCIFFALVGIPNLNVVLNRLGHLMQQGVNH--WASRLGGTWQDPDKAR
h TASK2      GNVAPKTPAGRLFCVFGYGLFVPLCLTWISALGKFFGGRAKR--LGQFLTGRGVSLRKAQ
hTWIK-1      GHTVPLSDGGKAFCIYISVIGIPFTLLFLTAVVQRITVHVTRRPVLYFHIRWGFQKQVVA
hTASK        GHAAPSTDGGKVFCMFYALLGIPLTLVMFQSLGERINTLVRY-LLHRAKKGLGMRRADVS
                *: * : :.: **: :.: *: * : : : :
                        TM 3
Athua133f10  WLAGSGALLSGLLLFLLLPLLFSHMEG-WSYTEGFYFAFITLSTVGFGDYVIG-MNPSQ
h TASK2      ITCTVIFIVWGVLVHLVIPPFVFMVTEG-WNYIEGLYYSFITISTIGFGDFVAG-VNPSA
hTWIK-1      IVHAVLLGFVTVSCFFFIIPAAVFSVLEDDWNFLESFYFCFISLSTIGLGDYVPG-EGYNQ
hTASK        MANMVLIGFFSCISTLCIGAAAFSHYEH-WTFFQAYYYCFITLTTIGFGDYVALQKDQAL
                .   : : . *   *   *: :. :. *: :.: :.: :.: :.: :.: :
                        TM 4
Athua133f10  RYPLWYKNMVSLWLIFGMAWLALIILKILLSQLETPGRVCSCCHHSSKEDFKS-----
h TASK2      NYHALYRYFVELWIYLGWLWLSLFDVNWKVSMFVEVHKAIKRRRRRRKESFESSPHSRKAL
hTWIK-1      KPRELYKIGITCYLLGLLIAM-LVVLETFCELHELKFKRKMFFVKKDKDEDQ-----
hTASK        QTPQYVAFSFFVYILTGLTVIGAFLNLVVLRFMTMNAEDEKRDAAEHRALLTRNG-----
                .   *   : : * : : :. :   :   :
Athua133f10  -----QSWRQGPDPREPESHSPQQGCYPEG
h TASK2      QVKGSTASKDVNIFSFSLKKEETYNDLIKQIGKKAMKTSGGGETGPGPGLGPQGGGLPAL
hTWIK-1      -----VHIIEHDQLSFSSITDQAAGMKED
hTASK        Q-----AGGGGGGSAHTTDTASSTAAAGGGG
                :
Athua133f10  PMGIIQHLEPSAHAAGCGKDS-----
h TASK2      PPSLVPLVVYSKNRVPTLEEVSQTLRSKGHVSRSPDEEAVARAPEDSSPAPEVFMNQLDR
hTWIK-1      QKQNEPFVATQSSACVDGPANH-----
hTASK        FRNVYAEVLHFQSMCSCLWYKSREKLQYSIPMIIPRDLSTSDTCVEQSHSSPGGGGRYSD
                :
Athua133f10  -----
h TASK2      ISEECEPWAQDYHPLIFQDASITFVNTEAGLSDEETSKSSLEDNLAGEESPQQGAEAKA
hTWIK-1      -----
hTASK        TPSRRCLCSGAPRSAISSVSTGLHSLSTFRGLMKRRSSV-----
Athua133f10  -----
h TASK2      PLNMGEFPSSSESTFTSTESLSVPYEQLMNEYNKANS PKGT
hTWIK-1      -----
hTASK        -----
```

Fig. 9

13/26

GAP of: twik2.pep check: 1565 from: 1 to: 499

TWIK2 FthKa20g4

to: twik3.pep check: 8445 from: 1 to: 332

TWIK3 Athua133f10 - jthua133f10, 1575 bases, 18 checksum.

Symbol comparison table:
/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight:	12	Average Match:	2.912
Length Weight:	4	Average Mismatch:	-2.003
Quality:	396	Length:	517
Ratio:	1.193	Gaps:	3
Percent Similarity:	40.764	Percent Identity:	32.166

Match display thresholds for the alignment(s):

	=	IDENTITY
:	=	2
.	=	1

twik2.pep x twik3.pep

```

1 .....MVDRGPLLTSaiIFyLAIGAAIFEVLEEPHWKE 33
1 MYRPRARAAPEGRVRCaVPGTVLLLLaYLaYLaLGtGVFWtLEGRAAQD 50
34 AKNYYTQKLHLLKEFPCLGQEGLDKILEVVSdAAGQGVaITGNQT.FNN 82
51 SSRSFQRDKWELLQNFtCLDRPaLDSLiRDVvQAYKNGASLLSNTtSMGR 100
83 WNWPNAMiFAATViTTiGYGNVAPKtPaGRlFCVfYGLFGVPLCLtWiSA 132
101 WELVGSFFFSVStiTTiGYGNLSpNTMaARlFCiFFaLVGIPLNLVVLNR 150
133 LGKFFGGRAKRLGQFLTKRGVSLRKAQITCTViFiVWGVLVHLViPPFVF 182
151 LGHLMQQGVNHWASRLGGTWQDPDKARWLAGSGALLSGLLLFLLLPPLLF 200
183 MVTEGWNYIEGLYYSFiTiStiGFgDFVAGVNPSANYHaLYRYfVELWiy 232
201 SHMEGWSYTEGFYFAFiTLStVGfGDYViGMNPSQRYPLWYKNMVSLWIL 250
233 LGLAWLSLfvNWKVSMFVEVhKaIKRRRRRRKESFESSPhSRKaLQVKGS 282
251 FGMAWLALIiKLILSQLETPGRVCSCCHSSKEDFKSQSW.RQGPDRPE 299
283 TASKDVNiFSFLSKKEETyNDLiQIGKkAMKtSGGGETGPGPGLGpQGG 332
300 SHSPQQGCY.....PEGPMGiIQHLEPSaHAAGCGKDS..... 332

```

Fig. 10

```

1  .MRRGALLAGALAAAYAAYLVLGALLVARLEGPHEARLRAELET LRAQLLQ 49
   . | | | | | : | | : | | : | | | | : | | | |
1  MVDRGPLLTSAI...IFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLK 47
   . | | . | | | | | | | | | | | | | | | | | | |
50 RSPCVAAPALDAFVERVLAAGRLGRVVLANASGSANASDPAWDFASALFF 99
   | | . | | | | | | | | | | | | | | | | | | |
48 EFPCLGQEGLDKILEVVS DAAGQGVAITGNQTFN.....NWNWPNAMIF 91
   . | | . | | | | | | | | | | | | | | | | | | |
100 ASTLITTVGYGYTTPLTDAGKAFSIAFALLGVPTTMLLLTASAQRLSLLL 149
   | . | . | | | | | | | | | | | | | | | | | | |
92 AATVITTIGYGNVAPKTPAGRLFCV FYGLFGVPLCLTWISALGKFFGGRA 141
   . | | . | | | | | | | | | | | | | | | | | | |
150 THVPLSWLSMRWGWDPRRAACWHLVALLGVVVTVCF LVPÄVIFAHLEEAW 199
   | | | | | | | | | | | | | | | | | | | | | |
142 KR..LGQFLTKRGVSLRKAQITCTVIFIVWGV LVHLVIPPFVFM.VTEGW 188
   . | | . | | | | | | | | | | | | | | | | | | |
200 SFLDAFYFCFISLSTIGLGDYVPGEAPGQPYRALYKVLVTVYLFLGLVAM 249
   . : : : | : | | . : | | | | | | | | | | | | | | |
189 NYIEGLYYSFITISTIGFGDFVAGVNPSANYHALYRYFVELWIY LGL.AW 237
   . | | . | | | | | | | | | | | | | | | | | | |
250 VLV LQTFRHVSDLHGLTELILLPPPCPASFNAD EDDRVDILGPQPE SHQQ 299
   . . . . : | | | | | | | | | | | | | | | | | | |
238 LSLFVNWKVSMFVEVHKAIKRRRRRRRKESFESSPHSRKALQVKGSTASKD 287
   . | | . | | | | | | | | | | | | | | | | | | |
300 LSASSHTDYASIPR..... 313
   . : | | . | | | | | | | | | | | | | | | | | | |
288 VNIFSFLSKKEETYNDLIKQIGKKAMKTS GGGETGPGPGLGPOGGGLPAL 337
   . | | . | | | | | | | | | | | | | | | | | | |

```

15/26

GAP of: twik3.pep check: 8445 from: 1 to: 332
TWIK3 Athua133f10 - jthua133f10, 1575 bases, 18 checksum.
to: twik4.pep check: 9188 from: 1 to: 313
TWIK4 AthTb005e07 - jthTb005e07, 2287 bases, 4935 checksum.

Symbol comparison table:
/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight:	12	Average Match:	2.912
Length Weight:	4	Average Mismatch:	-2.003
Quality:	257	Length:	345
Ratio:	0.821	Gaps:	7
Percent Similarity:	40.333	Percent Identity:	31.667

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1

twik3.pep x twik4.pep..

```

1 MYRPRARAAPEGRVRCVAVPGTVLLLLLAYLAYLALGTGVFWTLEGRAAQD 50
1 .....MRRGALLAGA...LAAYAAYLVLGALLVARLEGPHEAR 35
51 SSRSFQRDKWELLQNFCTCLDRPALDSLIRDVVQAYKNGASLLSNTTSMGR 100
36 LRAELET LRAQLLQRSPCAAPALDAFVERVLAAGRLGRVVLANASGSAN 85
101 .....WELVGSFFFSVSTITTIGYGNLSPNTMAARLFCIFFALVGIPLNL 145
86 ASDPAWDFASALFFASTLITTVGYGYTTPLTDAGKAFSIAFALLGVPTTM 135
146 VVLNRLGHLMQQGVNHW.ASRLGGTW.QDPDKARWLAGSGALLSGLLLFL 193
136 LLLTASAQRLSLLLTHVPLSWLSMRGWDPRAACWHLVALLGVVTVCF 185
194 LLPPLLF SHM.EGWSYTEGFYFAFITLSTVGFGDYVIGMNPSQRYPLWYK 242
186 LVPVIFAHLEEAWSF LDAFYFCFISLSTIGLDYVPGEAPGPYRALYK 235
243 NMVSLWILFGMAWLALIILKILS QLETPG.....RVCSCCHHSSKEDFKS 287
236 VLVTVYLFLGLVAMVLVLQTFRHVSDLHGLTELILLPPPCPASFNADDD 285
288 QSWRQGPDPREPESHSPQQGCYPEGPMGIIQHLEPSAHAAGCGKDS 332
286 RVDILGP..QPESHQQLSASSHTDYASIPR..... 313

```

Fig. 12

GAP of: htwik-1.pep ch ck: 4093 from: 1 to: 336

hTWIK-1 U33632 Human two P-domain K+ channel TWIK-1 mRNA, complete cds.

to: twik2.pep check: 1565 from: 1 to: 499

TWIK2 FthKa20g4

Symbol comparison table:
/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 269 Length: 521
Ratio: 0.801 Gaps: 4
Percent Similarity: 36.943 Percent Identity: 26.433

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

htwik-1.pep x twik2.pep

```
1 MLQSLAGSSCVRLVERHRSAWCFGLVLGYLLYL VFGAVVFSSVELPYED 50
1 .....MVDRGPLLTS AIFYLAIGAAIFEVLEEPHWK 32
51 LLRQELRKLKRRFLEEHECLSEQQLEQFLGRVLEASNYGVSVLSNASGNW 100
33 EAKKNYYTQKLHLLKEFPCLGQEGLDKILEVVSDAAGQGVAITGNQTFN. 81
101 NWDFTSALFFASTVLSTTGYGHTVPLSDGGKAF CIIYSVIGIPFTLLFLT 150
82 NWNWPNAMIFAATVITTIGYGNVAPKTPAGRLFCV FYGLFGVPLCLTWIS 131
151 AVVQRITVHVTRRPVLYFHIRWGF SKQVVAIVHAVLLGFVTVSCFF FIPA 200
132 ALGKFFGGRKR..LGQFLT KRGVSLRKAQITCTVIFIVWGVLVHLVIP P 179
201 AVFSVLEDDWNFLESFYFCFISLSTIGLGDYVP GEGYNQKFRELYKIGIT 250
180 FVFMVTE.GWNYIEGLYYSFITISTIGFGDFVAG VNP SANYHALYRYFVE 228
251 CYLLLGL..IAMLVVLETFCELHELKKFRKM FYVKKDKDEDQVHII EHDQ 298
229 LWIYLGAWLSL FVNWKVSMFVEVHKA IKRRRRRKESFESSPHSRKALQ 278
299 LSFSSITDQAAGMKEDQKQNEP FVATQSSACVDGPANH..... 336
279 VKGSTASKDVNIFSLSKKEETYNDLIKQIGKKAM KTSGGGETGPGPGLG 328
```


17/26

GAP of: htwik-1.pep check: 4093 from: 1 to: 336

hTWIK-1 U33632 Human two P-domain K+ channel TWIK-1 mRNA, complete cds.

to: twik3.pep check: 8445 from: 1 to: 332

TWIK3 Athua133f10 - jthua133f10, 1575 bases, 18 checksum.

Symbol comparison table:
/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 199 Length: 337
Ratio: 0.599 Gaps: 3
Percent Similarity: 31.420 Percent Identity: 22.961

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

htwik-1.pep x twik3.pep..

```

      1 MLQSLAGSSCVRLVERHRSÄWCFGLVLGYLLYL VFGAVVFSSVELPYED 50
      : . . . . . | . . . . . | . . . . . | . . . . . |
      1 .MYRPRARAAP EGRV RGC A V P G T V L L L L A Y L A Y L A L G T G V F W T L E G R A A Q 49

51 LLRQELRKLR RRFLEEHECLSEQQLEQFLGRVLEASNYGVSVLSNASGNW 100
      . . : | . . : | . . : | . . : | . . : | . . : | . . : |
50 DSSRSFQ RDKWELLQNF T C L D R P A L D S L I R D V V Q A Y K N G A S L L S N T T S M G 99

101 NWDFTSALFFASTV LSTTG Y G H T V P L S D G G K A F C I I Y S V I G I P F T L L F L T 150
      | : . . | | . . : | | | . | . : | | | : . . : | | | . |
100 RWELVGSFFF S V S T I T T I G Y G N L S P N T M A A R L F C I F F A L V G I P L N L V V L N 149

151 AVVQRITVHVTRRPVLYFHIRWGFSKQVVAIVHAVLLGFVTVSCFFFI PÄ 200
      | . . . . . | . . . . . | . . . . . | . . . . . |
150 RLGHLMQQGVNHWASRLGGTWQDPDKARWLAGSGALLSGLLL..FLLLPP 197

201 AVFSVLEDDWNFLESFYFCFISLSTIGLDYVPGE GYNQKFRELYKIGIT 250
      . | | : | | . : | | | | | . | | | : | | | | | . | : : | | : .
198 LLFSHME.GWSYTEGFYFAFITLSTVGF GDYVIGMNP S QRYPLWYKNMVS 246

251 CYLLLGLIAMLVVLE.TFCE LHELKKFRKMFYVKKDKDEDQVHII EHDQ L 299
      : : | | : : : . : | . : : . | . : : . | . : : . |
247 LWILFGMAWLALI I K L I L S Q L E T P G R V C S C H H S S K E D F K S Q S W R Q G P D R 296

300 SFSSITDQAÄGMKEDQKQNEPFVATQSSACVDGPANH 336
      | . | . | . | . | . | . | . | . | . | . | . | . |
297 EPESHSPQQGCYPEGPMGIIQHLEPSAHAAGCGKDS. 332

```

Fig. 14

18/26

GAP of: htwik-1.pep check: 4093 from: 1 to: 336

htwik-1 U33632 Human two P-domain K⁺ channel TWIK-1 mRNA, complete cds.

to: twik4.pep check: 9188 from: 1 to: 313

TWIK4 AthTb005e07 - jthTb005e07, 2287 bases, 4935 checksum.

Symbol comparison table:
/usr/local/gcg_9.1/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight: 12 Average Match: 2.912
Length Weight: 4 Average Mismatch: -2.003

Quality: 575 Length: 353
Ratio: 1.837 Gaps: 4
Percent Similarity: 55.405 Percent Identity: 46.284

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

htwik-1.pep x twik4.pep..

```

1 MLQSLAGSSCVRLVERHRSÄWCFGLVLGYLLYLVFHAVVFSSVELPYED 50
  | | | | | | | | | | | | | | | | | | | | | | | | | |
1 .....MRRGALLAGALA.AYAAYLVLGALLVARLEGPHEA 34
  | | | | | | | | | | | | | | | | | | | | | | | | | |
51 LLRQELRKLRKFLEEHECLSEQQLEQFLGRVLEASNYGVSVLSNASGNW 100
  | | | | | | | | | | | | | | | | | | | | | | | | | |
35 RLRAELETLRAQLLQSPCVAAPALDAFVERVLAAGRLGRVVLANASGSA 84
  | | | | | | | | | | | | | | | | | | | | | | | | | |
101 N.....WDFTSALFFASTVLSTTGYGHTVPLSDGGKAFCCIYSVIGIPFT 145
  | | | | | | | | | | | | | | | | | | | | | | | | | |
85 NASDPAWDFASALFFASTLITTVGYGYTTPLTDAGKAFSIAFALLGVPTT 134
  | | | | | | | | | | | | | | | | | | | | | | | | | |
146 LLFLTAVVQRITVHVTRRPVLYFHIRWGFQVVAIVHAVLLGFVTVSCF 195
  | | | | | | | | | | | | | | | | | | | | | | | | | |
135 MLLLTASAQRLSLLLTHVPLSWLSMRWGWDPRAACWHLVALLGVVTVTC 184
  | | | | | | | | | | | | | | | | | | | | | | | | | |
196 FFIPAAVFSVLEDDWNFLESFYFCFISLSTIGLDYVPGEQYNQKFRELY 245
  | | | | | | | | | | | | | | | | | | | | | | | | | |
185 FLVPAVIFAHLEEAWSFDAFYFCFISLSTIGLDYVPGEAPGQPYRALY 234
  | | | | | | | | | | | | | | | | | | | | | | | | | |
246 KIGITCYLLGLIAMLVVLETFCHELHELKFRKMFYVK.....KDKDE 288
  | | | | | | | | | | | | | | | | | | | | | | | | | |
235 KVLVTVYLFLGLVAMVLVLQTFRHVSDLHGLTELILLPPPCPASFNADED 284
  | | | | | | | | | | | | | | | | | | | | | | | | | |
289 DQVHII.....EHDQLSFSSITDQAAGMKEDQKQNEPFFVATQSSACVDGP 333
  | | | | | | | | | | | | | | | | | | | | | | | | | |
285 DRVDILGPQPESHQQLSASSHTDYASIPR..... 313

```

Fig. 15

1	MVDRGPLLTSAAIFFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLKEFP	50
1	MVDRGPLLTSAAIFFYLAIGAAIFEVLEEPHWKEAKKNYYTQKLHLLKEFP	50
51	CLGQEGLDKILEVVSDAAGQGVAITGNQTFNNWNWPNAMIFAATVITTIG	100
51	CLGQEGLDKILEVVSDAAGQGVAITGNQTFNNWNWPNAMIFAATVITTIG	100
101	YGNVAPKTPAGRLFCVFGYGLFGVPLCLTWISALGKFFGGRAKRLGQFLTK	150
101	YGNVAPKTPAGRLFCVFGYGLFGVPLCLTWISALGKFFGGRAKRLGQFLTK	150
151	RGVSLRKAQITCTVIFIVWGVLVHLVIPPFVFMVTEGWNYIEGLYYSFIT	200
151	RGVSLRKAQITCTVIFIVWGVLVHLVIPPFVFMVTEGWNYIEGLYYSFIT	200
201	ISTIGFGDFVAGVNPSANYHALYRYFVELWIYLGAWLSLFDVNWKVSMFV	250
201	ISTIGFGDFVAGVNPSANYHALYRYFVELWIYLGAWLSLFDVNWKVSMFV	250
251	EVHKAIAKRRRRRRESFESSPHSRKALQVKGSTASKDVNIFSFLSKKEET	300
251	EVHKAIAKRRRRRRESFESSPHSRKALQVKGSTASKDVNIFSFLSKKEET	300
301	YNDLIQIQIGKKAMKTSGGGETGPGPGLGPGGGGLPALPPSLVPLVVYSKN	350
301	YNDLIQIQIGKKAMKTSGGGETGPGPGLGPGGGGLPALPPSLVPLVVYSKN	350

```

      .       .       .       .
351 RVPTLEEVSQTLRSKGHVSRSPDEEAVARAPEDSSPAPEVFMNQLDRISE 400
    |||||
351 RVPTLEEVSQTLRSKGHVSRSPDEEAVARAPEDSSPAPEVFMNQLDRISE 400
      .       .       .       .
401 ECEPWDAQDYHPLIFQDASITFVNTEAGLSDEETSKSSLEDNLAGEESPQ 450
    |||||
401 ECEPWDAQDYHPLIFQDASITFVNTEAGLSDEETSKSSLEDNLAGEESPQ 450
      .       .       .       .
451 QGAEAKAPLNMGEFPSSSESTFTSTESELSVPYEQLMNEYNKANSPKGT 499
    |||||
451 QGAEAKAPLNMGEFPSSSESTFTSTESELSVPYEQLMNEYNKANSPKGT 499

```

Fig. 16 (continued)

>human TWIK 5

CTAGGGAGGGCGCCATCTGAGTAGTTCGGAAGAACTGAACATGATGAGTT
GCCGGCTGCTTCCTGAGTCCTTGGGGAAGCACACGCACCATCCACTTAGC
ACTGGAGCCTGGCTGTTCTCCGGGCACTCCTACCCCATCTTCCTGGCGGG
GCTTAGATGCTCCTGCCTCTTCCACCAGCTCCTCTTGCCCTGCATGCTTC
AGGGACGATGGAGGTCTCGGGGCACCCCCAGGCCAGGAGATGCTGCCCAG
AGGCCCTGGGAAAGCTCTTCCCTGGCCTCTGCTTCCTCTGCTTTCTGGTG
ACCTACGCCCTGGTGGGTGCTGTGGTCTTCTCTGCCATTGAGGACGGCCA
GGTCTGGTGGCAGCAGATGATGGAGAGTTTGAGAAGTTCTTGAGGAGAGC
TCTGCAGAATCTTGAAC TGCAGTGAAACAGTGGTGGAGACAGAAAACAG
GATCTCCAGGGGCATCTGCAGAAGGTGAAGCCTCAGTGGTTTAACAGGAC
CACACACTGGTCCTTCTGAGCTCGCTCTTTTTCTGCTGCACGGTGTTCA
GCACCGTGGGCTATGGCTACATCTACCCCGTCACCAGGCTTGGCAAGTAC
TTGTGCATGCTCTATGCTCTCTTTGGTATCCCCCTGATGTTCTCGTTCT
CACGGACACAGGCGACATCCTGGCAACCATCTTATCTACATCTTATAATC
GGTTCCGAAAATTCCCTTTCTTTACCCGCCCCCTCCTCTCCAAGTGGTGC
CCCAAATCTCTCTTCAAGAAAAAACCGGACCCCAAGCCCGCAGATGAAGC
TGTCCCTCAGATCATCATCAGTGCTGAAGAGCTTCCAGGCCCCAACTTG
GCACATGTCCTTCACGCCCAAGCTGCAGCATGGAGCTGTTTGAGAGATCT
CATGCGCTAGAGAAACAGAACACACTGCAACTGCCCCCACAAGCCATGGA
GAGGAGTAACTCGTGTCCCGAACTGGTGTGGGAAGACTCTCATACTCCA
TCATCAGCAACCTGGATGAAGTTGGACAGCAGGTGGAGAGGTTGGACATC
CCCCCTCCCCATCATTTGCCCTTATTGTTTTTGCTACATTTCTGTGCAGC
TGCCATCCTCCCCTTCTGGGAGACACAGTTGGATTTGAGAAATGCCTTCT
ATTTCTGCTTTGTACACTCACCACCATTGGGTTTGGGGATACTGTTTTA
GAACACCCTAACTTCTTCTGTTCTTCTCCATTTATATCATCGTTGGAAT
GGAGATTGTGTTTATTGCTTTCAAGTTGGTGCAAAACAGGCTGATTGACA
TATACAAAAATGTTATGCTATTCTTTGCAAAAGGGAAGTTTTACCACCTT
GTTAAAAAGTGAAGGTTTCATTATCTCTCAGGTGACAGACACTGGCTGAG
CTGGTTTTCTGTGTTGTCTTTCAGGGTCATGCAGCCTGTCACCTGAGAC
CTTCAGTCTTGGAGACAAATCCCTTATGAGAGCCAAGTTCAGTCTTGAGG
CCCTGC

MLLPLPPAPLALHASGTMEVSGHPQARRCCPEALGKLFPGLCFLCFLVITYALVGAVV
FSAIEDGQVLVAADDGEFEKFLLEELCRILNCSETVVEDRKQDLQGH LQKVKPQWFNR
TTHWSFLSSLFFCCTVVFSTVGYGYIYPVTRLGKYLCMLYALFGIPLMFLVLTDTGDI
LATILSTS YNFRKFPFFTRPLLSKWCPSLFFKKKPD PKPADEAVPQIIISAEELPG
PKLGTCP SRPSCSMELFERSHALEKQNTLQLPPQAMERSNSCP ELVLGRLSYSIISN
LDEVGQQVERLDIPLPIIALIVFAYISCAAAILPFWETQLDFENAFYFCFVTLTTIG
FGDTVLEHPNFFLFFSIYIIVGMEIVFIAFKLVQNRLIDIYKNVMLFFAKGKFYHLV
KK

Fig. 17

22/26

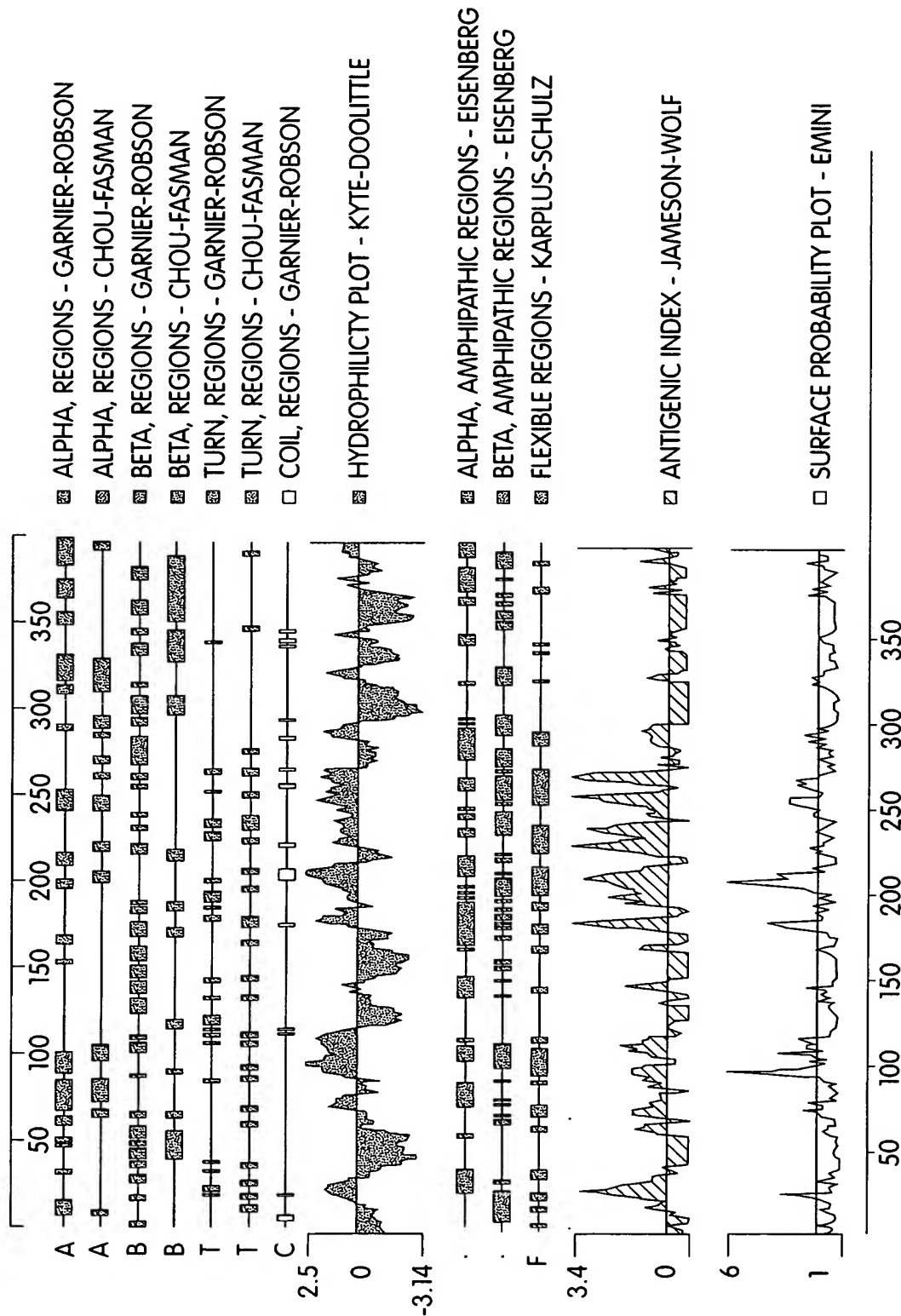


Fig. 18

23/26

GAP of: ORBa005gy ch ck: 9848 from: 1 to: 401

TWIK-5 protein (analysis onl - Import - compl t

to: PRBa005gy check: 4672 from: 1 to: 394

2465542 in GenPept

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/PAM250
CompCheck: 5553

Gap Weight:	25	Average Match:	2.617
Length Weight:	1	Average Mismatch:	-3.416
Quality:	166	Length:	538
Ratio:	0.421	Gaps:	5
Percent Similarity:	49.805	Percent Identity:	29.183

Match display thresholds for the alignment(s):

| = IDENTITY
: = 2
. = 1

ORBa005gy x PRBa005gy

```

1 MLLPLPPAPIALHASGTMEVSGHPQARRCCPEALGKLFPGLCFLCFLVTY 50
1 .....MKRQNVRTLALIVCTFTY 18
51 ALVGAVVFSAIEDGQVLVAADDGEFEKFLLEELCRILNCSETVVEDRKQDL 100
19 LLVGAAVFDALASEPELIERQRLELRQ.....QELRARYNLSQGGYEEL 62
101 QGHLQKVKPQWFNRTTHWSFLSSLFFCCTVFSTVGYGYYIPVTRLGKYLC 150
63 ERVVLRLKPH..KAGVQWRFAGSFYFAITVITTIGYGHAAPSTDGGKVFC 110
151 MLYALFGIPLMFLVLTDTGDILATILSTSYNRFRKFPFFTRPLLSKWCPK 200
111 MFYALLGIPLTLVMFQSLGERINTLVRYLLHRAK..... 145
:
:
251 LEKQNTLQLPPQAMERSNSCPVLGRLSYSIISNLDEVGOQVERLDIPL 300
146 .....GLGMRRADVSM 156
301 PIALIVF...AYISCAAAILPFWETQLDFENAFYFCFVTLTTIGFGD.. 345
157 ANMVLIGFFSCISTLCIGAAAFSHYEHWTFFQAYYYCFITLTTIGFGDYV 206
346 .....TVLEHPNFFLFFSIYIIVGMEIVFIAFKLVQNRLLIDIYKNVMLF 389
207 ALQKDQALQTQPQYVAFSIFYILTGLTVIGAFNLVVLRFMTMNAEDEKR 256
390 FAKGKFYHLVKK..... 401
257 DAEHRALLTRNGQAGGGGGGSAHTTDTASSTAAAGGGGFRNVYAEVLHF 306

```

Fig. 19

24/26

GAP of: GRBa005gy ch ck: 9848 from: 1 to: 401
TWIK-5 prot in (analysis onl - Import - complet
to: HRBa005gy check: 2856 from: 1 to: 426
4101566 in GenPept

Symbol comparison table: /prod/ddm/seqanal/BLAST/matrix/aa/PAM250
CompCheck: 5553

Gap Weight: 25 Average Match: 2.617
Length Weight: 1 Average Mismatch: -3.416
Quality: 77 Length: 563
Ratio: 0.192 Gaps: 6
Percent Similarity: 44.697 Percent Identity: 27.273

Match display thresholds for the alignment(s):
= IDENTITY
: = 2
. = 1

GRBa005gy x HRBa005gy

```

1 .....MLLPLPPAPLALHASGTM 18
1 MLPSASRERPGYRAGVAAPDLLDPKSAAQNSKPRLSFSTKPTVLASRVES 50
19 EVSGHPQARRCCPEALGKLFPGLCFLCFLVITYALVGAVVFS AIEDGQVLV 68
51 DTTINVMKWKT VST.....IFLVVVL YLIIGATVFKALEQPHEIS 90
69 AADDGEFEK..FLEELCRI LNCSETVVEDRKQDLQGH LQKV KPW FNR TT 116
91 QRTTIVIQKQTFISQHS CVNSTELDELIQQIVAAINAGI IPLGNTSNQIS 140
117 HWSFLSSLFFCCTV FSTVGYGYIYPVTRLGKYLCMLYALFGIPLMFLVLT 166
141 HWDLGSSFFFAGTVITTIGFGNISPRTEGGKIFCIIYALLGIPLFGFLLA 190
167 DTGDILATILSTSYNRFKFPFFTRP LLSKWCPKSLFKKKPDPKPADEAV 216
191 GVGDQLGTIFGKG..... 203
:
267 SNSCPVLVLR LSYSIISNLDEVGQQVERLDIPLPIIALIVFAYISCA.. 314
204 .....IAKVEDTFIKWNVSQTKIRIISTIIIFILFGCVLF 237
315 ...AAILPFWETQLDFENAFYFCFVTLTTIGFGDTVLEHPNFFLFFSIYI 361
238 VALPAIIFKHIEGWSALDAIYFVVITLTTIGFGD.....YV 273
362 IVGMEIVFIAFKLVQNRLIDIYKNVMLFFAKGKFYHLVKK..... 401
274 AGGSDIEYLDF.....YKPVVWFVILVGLAYFAAVLSMIGRLVRV 313
:

```

Fig. 20

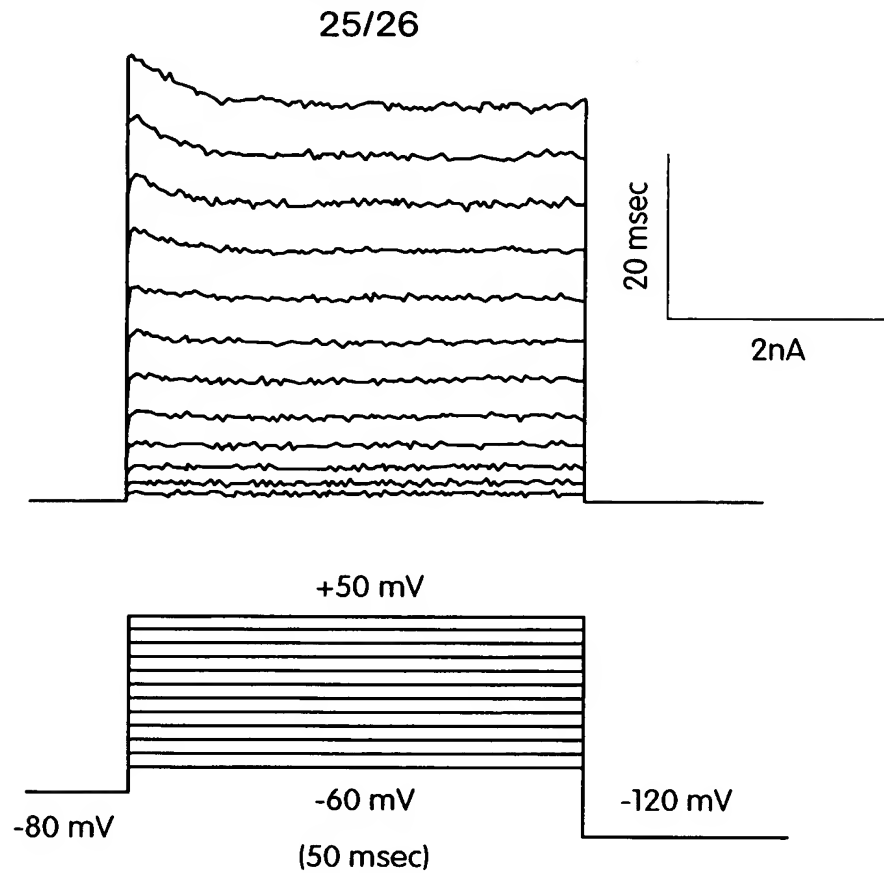


Fig. 21A

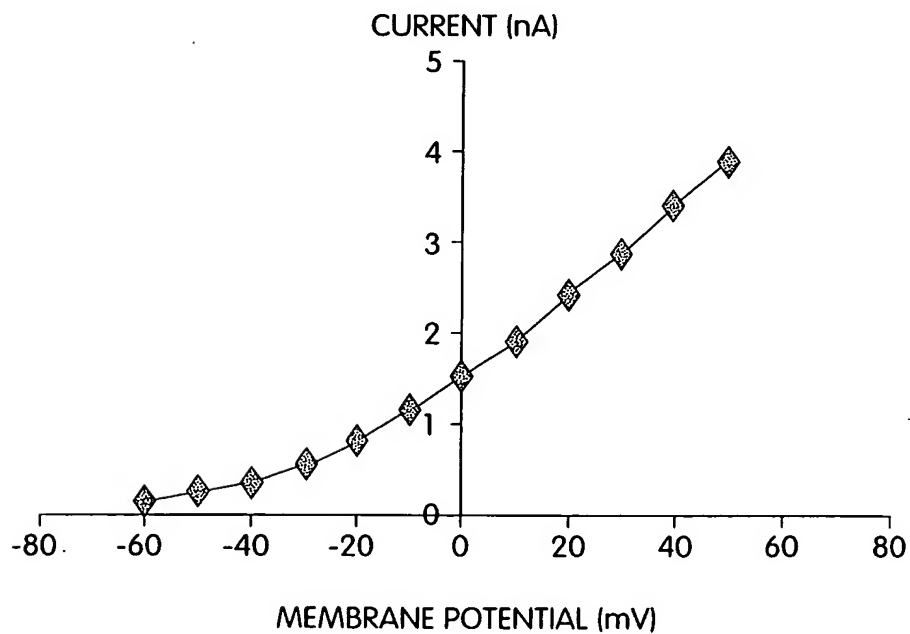


Fig. 21B

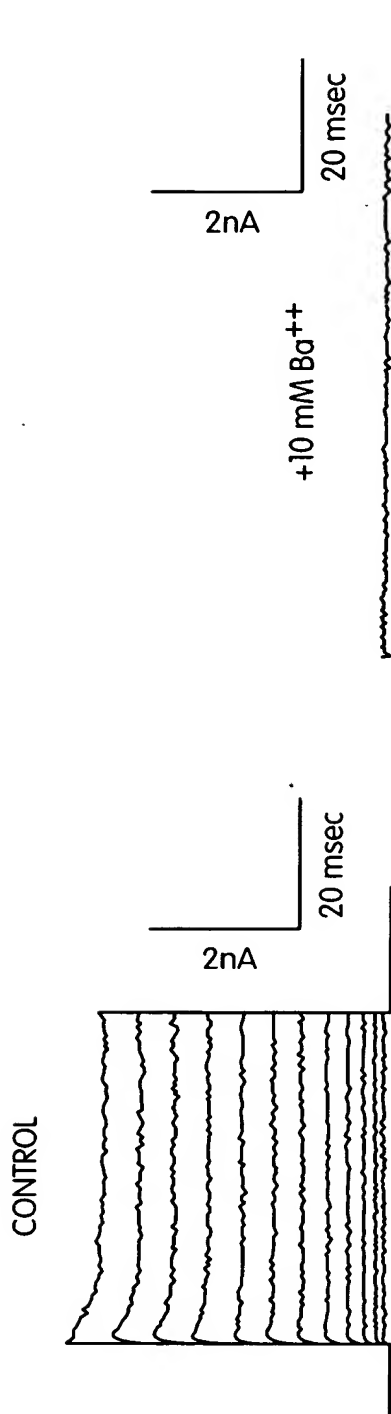


Fig. 22A

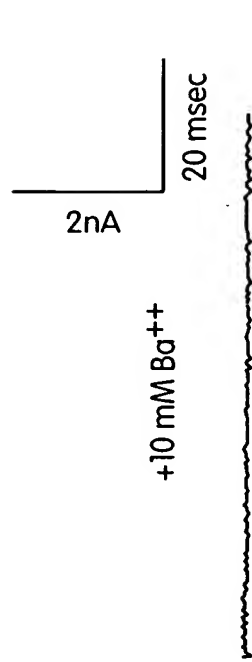


Fig. 22B

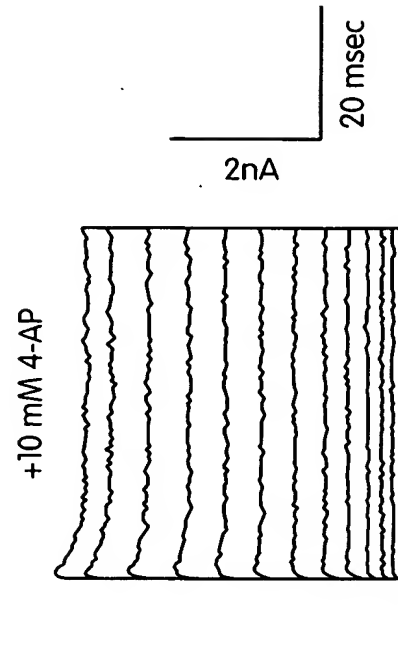


Fig. 22D



Fig. 22C